

PROTEOMIC INTERACTION ARRAYS

ABSTRACT OF THE DISCLOSURE

A method is provided for the rapid identification of protein-protein interaction networks within a cell, tissue, or whole genome. The introduction of a multi-bait approach is a distinguishing feature of the technology. In this method a pair of two-hybrid cDNA libraries, each one carrying the complement of genes from the tissue under study, are combined for an interaction screen. A large number of yeast colonies, each identifying a protein interaction pair, are picked and distributed in single wells, providing an arrayed archive of protein-protein interactions. The archive also serves as a source of plasmids to construct arrayed replicas containing DNA of the interacting plasmid pairs. Hybridization of a given cDNA to the arrayed replicas identifies the corresponding interacting clones. Protein interaction networks are constructed by iteration of the hybridization with newly identified interacting clones.